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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                    Score
    57
57
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Query
Match Length DB
    SPTREMBL_17:*
1: sp_archea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    January 30, 2002, 11:51:58; Search time 50.08 Seconds (without alignments) 40.891 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyright (c) 1993 -
                                                                                                                                                                                                                                                                                                                                                                                                    sp_archea:*
sp_bacteria:*
sp_fungi:*
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                                                                                                                                                                                                                                                                                                                                         sp_organelle:*
sp_phage:*
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sp_vertebrate:*
sp_unclassified:*
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    1662
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Q9KFN3
Q9SNN3
Q9FG26
                                                                                          Q9Y0E8
Q9I5M4
                                                                                 Q9Y7V5
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                               Q40548
Q08195
Q08194
Q9SJZ8
Q9SG73
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2000 Compugen Ltd.
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                                                                                                           Q9bu12 homo sapien
Q91qn0 arabidopsis
O80790 arabidopsis
O82276 arabidopsis
                                                                                                                                                   P71431 leptothrix
Q9kfn3 bacillus ha
Q9snn3 oryza sativ
Q9fg26 arabidopsis
040548 nicotiana t

068195 nicotiana t

068194 nicotiana t

098128 arabidopsis

056073 hepatitis g

0990m4 human coron

0990m2 human coron
                                                                              Q9y0e8 drosophila
Q9i5m4 pseudomonas
Q9y7v5 trichoderma
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45 47 4	44 47 4	43 47.5 4	42 47.5 4	41 48 4	40 48 4		38 48 4	37 48 4	36 49 4	35 49 4	34 49 4	33 49 4				49	49	49.5	26 49.5 4	50	50	50.5	50.5	51	20 51 4
5.6	5.6	6.1	6.1	6.6	6.6	46.6	6.6	6.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6				48.1				•		9.5
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Q9vx67 drosophila	Q9rwq6 deinococcus	Q9kqw8 vibrio chol	0	Q91p05 arabidopsis		Q9zuy7 arabidopsis	Q9p0t8 homo sapien	Q91p00 arabidopsis	Q9v1p5 drosophila	Q9bxx0 homo sapien	Q9jh31 tt virus. o	O18300 caenorhabdi		Q19573 caenorhabdi	052853 bacillus su	Q9y9q4 aeropyrum p	Q9kzt3 streptomyce	Q9duc4 tt virus. o	Q56924 yersinia en	Q9av15 oryza sativ	Q9wyfl thermotoga	044626 caenorhabdi	Q9czal mus musculu	Q84712 porcine epi	Q990m1 human coron

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                                                                                                                                                                                                                      Q9SNN3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL PROTEIN.
Oryza sativa (Rice).
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 236 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases EMBL/-AP000559; BAA84796 l; - CRDASSARRDOODED CECA.
                                                                                                       "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, clone:P0493C11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
EMBL; AP001508; BAB04165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KFN3;
                                                                                                                                  Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                             STRAIN-CV. NIPPONBARE;
                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                       Q9SNN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH0446
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                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=4530
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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77.8%;
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Last annotation update)
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Pred. No.
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                                                                  282A558ED22DE9
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                          DB 10; Length 165;
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RESULT
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    Ö9FG26;
    O1-MAR-2001 (TrEMBLrel. 16, Created)
    O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
    O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
    NON-LTR RETROELEMENT REVERSE TRANSCRIPTASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC002960; AAH02960.1; - SEQUENCE 491 AA; 53836 MW; 15D07E714F592C9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP002032; BAB09815.1; -. RNA-directed DNA polymerase. SEQUENCE 676 AA; 76665 MW; AD1CC1E18E46F53A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FG26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=LUNG CARCINOMA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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Pred. No. 1
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                                                                                                                                                                                                                                                                              DB 4; Length 491;
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Best Local :
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STRAIN=CV. COLUMBIA;

Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,

Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,

Symerville C.R., Venter J.C.;

"Arabidopsis thaliana chromosome II BAC T12J2 genomic sequence.";

"Arabidopsis thaliana chromosome II BAC T12J2 denomic sequence.";
                                                                                                                                                                                                          O80790 PRELIMINARY; PRT; 970 AA. 080790; O1-NOV-1998 (TREMBLrel. 08, Created) 01-NOV-1998 (TREMBLrel. 08, Last sequence update) 01-JUN-2001 (TREMBLREL. 17, Last annotation update) REVERSE-TRANSCRIPTASE-LIKE PROTEIN.
                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;
Liu S.X., Chan A., Yu G., Lee J.M., Lenz C., Pham P., Sakano H.,
Toriumi M., Vysotskaia V.S., Chin C., Chiou J., Choi E., Chung M.,
Gonzalez A., Howng B., Liu A., Vaysberg M., Altafi H., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F.,
Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
Tederspiel N.A., Theologis A.;
"The sequence of BAC F5D14 from Arabidopsis thaliana chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC007767; AAF81325.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                    59 RNWWWWPVLVITDVGGEWSWWWWPVL 85
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                2 RRWPWWP------WKWPLI 14
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Last sequence update)
Last annotation update)
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Pred. No.
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                                                                                                                                                          core eudicots; Rosidae;
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                                                                                                                                                                                                                                  Q9Y0E8;
Q9Y0E8;
01-NOV-1999
                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SALIVARY GLAND SECRETION PROTEIN (FRAGMENT).
SGS1 OR SGS-1 OR CG3047.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
  Ephydroidea; Dro
NCBI_TaxID=7227;
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InterPro; IPR000169; Thiolprot_act_site.
Pfam; PF00078; rvt; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
RNA-directed DNA polymerase.
SEQUENCE 1231 AA; 139476 MW; 5832FD600F342BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M. Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C. "Arabidopsis thaliana chromosome II BAC T16B12 genomic sequence. Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: TO RNA-DIRECTED DNA POLYMERASE (REVERSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             082276 PRELIMINARY; PRT; 082276; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1998 (TrEMBLrel. 08, Last sequent of the control 
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Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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RNA-directed DNA polymerase.
SEQUENCE 970 AA; 110578 MW;
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46.7%;
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46.7%;
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Pred. No. 45;
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Pred. No. 36;
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Best Local Similarity
"hes 6; Conserv
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XX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
XX Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
XX Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
XX Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
XX Hrody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
XX Brith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
XX Reizer J., Saier M.H., Hancock R.E.W., Larbig K.B., Larbig K
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Best Local :
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Q915M4;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Roth G.E., Wattler S., Bornschein H., Lehmann M., Korge G.;
Roth G.E., Wattler S., Bornschein H., Lehmann M., Korge G.;
Roth G.E., Wattler S., Bornschein H., Lehmann M., Korge G.;
Structure and regulation of the salivary gland secretion protein
Sgs-1 of Drosophila melanogaster.";
Sgs-1 of Drosophila melanogaster.";
Genetics 0:0-0(1999).
Genetics 0:0-0(1999).
EMBL; AF156228; AAD43808.1; -.
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InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
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CMP1.
                                                                                                                                                                               Q9Y7V5;
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                                      CONIDIOSPORE SURFACE PROTEIN.
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(TremBLrel. 16, Last sequence update)
(TremBLrel. 17, Last annotation update)
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Pred. No.
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Pred. No. 15;
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RESULT
Q40548
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Best Local
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SEQUENCE 1245 AA; 135824 MW; 3249C749AFAOCDF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q40548;
Q1-JAN-1998 (TrEMBLrel. 05, Created)
Q1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV, PETITE HAVANA; TISSUE-PISTIL;
STRAIN-CV, PETITE HAVANA; TISSUE-PISTIL;
MEDLINE-93005740; PubMed-1992607;
MEDLINE-93005740; PubMed-1992607;
MEDLINE-93005740; PubMed-1992607;
Mariani C.;
Goldman S., Pezzotti M., Seurinck J., Mariani C.;
Goldman S., Pezzotti M., Seurinck J., Mariani C.;
Tusue Strain-1lke proteins.";
Plant Cell 4:1041-1051(1992)
Plant Cel
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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SEQUENCE
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REPEAT
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Mendel; 16906; Nicta;2747;16906.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                       REPEAT
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43 WPWEIPCYLTWPFPWP 58
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                                             4 WPW---
                                                                                                              Similarity
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                                           ----WPWKWP 12
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81
81
93
105
                                                                                             Conservative
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109
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85
87
109
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62.5%;
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Pred. No.
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3 X 5 AA REPEATS OF S-P(4).
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Pred. No. 6.8;
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RESULT 13
Q08195
ID Q08195
AC Q08195
DT 01-NOV
DT 01-STEELIN
OC SPERMA
OC SPERMA
OC ASTEEL
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
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Proc.
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Q08194;
Q1-JAN-1998;
Q1-JAN-1998;
Q1-JUN-2000;
"Developmental expression of tobacco pistil specific genes encoding novel extensin-like proteins";
Plant Cell 4:1041-1051(1992).
-! TISSUE SPECIFICITY: PISTIL (STIGMA AND STYLE TISSUE).
-! DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN FLORAL BUDS AFTER PISTIL DIFFERENTIATION AND LEVELS GRADUALLY INCREASE DURING FLOWER DEVELOPMENT TOWARD ANTHESIS. LEVELS GRADUALLY DECREASE AFTER POLLINATION AND ARE ABSENT BY THE SIXTH DAY AFTER POLLINATION.
EMBL; 2143439: AAA34059.1; -.
Mendel; 16901; Nicta; 2747;16901.
Structural protein; Repeat; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-93342083; PubMed-8341705;

Wu H.M., Zou J., May B., Gu Q., Cheung A.Y.;

"A tobacco gene family for flower cell wall proteins with a rich domain and a cysteine-rich domain.";

Proc. Natl. Acad. Sci. U.S.A. 90:6829-6833(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TREMBLrel. 05, Created)
01-JAN-1998 (TREMBLrel. 05, Last sequence update)
01-JUN-2000 (TREMBLrel. 14, Last annotation update)
01-JUN-2000 (TREMBLRel. 14, Last annotation update)
PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR
(CYSTENE-RICH EXTENSIN-LIKE PROTEIN 1).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae. euasteride I. Schenbler (College).
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Q08195;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2000
                                                                                                                                                                                                                                                                SEQUENCE OF 39-209 FROM N.A.
STRAIN-CV. PETITE HAVANA; TISSUE-PISTIL;
MEDLINE-93005740; PubMed-1392607;
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"A tobacco gene family for flower cell wall proteins with a proline-
rich domain and a cysteine-rich domain.";
Proc. Natl. Acad. Sci. U.S.A. 90:6829-6833(1993).
EMBL; L13440; AAA34060.1;
Mendel; 16902; Nicta; 2747;16902.
SEQUENCE 196 AA; 21913 MW; 4C44E23C5B706E30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CYSTEINE-RICH EXTENSIN-LIKE PROTEIN 2.
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                Goldman S., Pezzotti M., Seurinck J., Mariani C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93342083; PubMed=8341705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Solanales; Solanaceae; Nicotiana.
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Pred. No. 11;
1; Mismatches
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Best Local Similarity
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Best Local
                                                Matches
                                                                                                                                STRAIN-CV. COLUMBIA;

MEDLINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

"Sequence and analysis of chromosome II of Arabidopsis thaliana.";

Nature 402:761-768(1999)

Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                O9SJZ8, PRELIMINARY; PRT; 321 AA.
O9SJZ8,
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                       RNA-directed DNA polymerase. SEQUENCE 321 AA; 36192 MW
                                                                                                                             EMBL; AC006592; AAD22368.1; -.
                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eeurosids II; Brassicales; Brassicaceae; Arabidopsis.
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REPEAT
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SEQUENCE
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DOMAIN
REPEAT
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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90
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                      4 WP-----WWPWKW 11
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WPTVFVMAVWWGWKW
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209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN 5 x 5 AA REPEATS OF S-P(4).
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                                                                                                       43736712301D41BA CRC64;
                                             Mismatches
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                                                         18;
                                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
                                                                   DB 10;
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                                                                                                                                                                                                                                                                                                                         core eudicots;
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                                                                   Length 321;
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